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CLAIM LISTING:

1.   (Currently Amended) A method for managing and analyzing information obtained from ~~differential~~ expression of genetic information in biological cells, the method comprising:

receiving sets of expression data derived from control and treatment sets of cell-derived samples as crisp input data, said sets of expression data representing a direction and a magnitude of regulation of each one of a higher number of different genes or proteins;

fuzzifying the crisp input data to provide fuzzified values;

applying a set of heuristic rules to the fuzzified values to generate a predicted value of a data point C;

defuzzifying the predicted value of C; and

determining a confidence level of the predicted value of C.

2.   (Original) The method of claim 1, further comprising:

filtering the crisp data to ensure the crisp data are above a predetermined noise level.

3.   (Original) The method of claim 2, wherein the applying of the set of heuristic rules is performed by using a decision matrix.

4.   (Original) The method of claim 2, wherein the determining of the confidence level of the predicted value of C comprises:

calculating a difference r between the defuzzified predicted value and an observed value of C; and

squaring r to provide r^2 and comparing r^2 to a predetermined value, a value of r^2 being smaller than the predetermined value indicating a high confidence level in the defuzzified predicted value of C.

5.   (Original) The method of claim 4, wherein the determining of the confidence level of the predicted value of C further comprises:

determining a distribution variance of the fuzzified values; and

obtaining a general score, for predicting credibility of decision matrix predictions, based upon the distribution variance and the value of r^2.

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6.   (Original) The method of claim 2, wherein the filtering comprises:

accepting the crisp input data only when one of the crisp input data having a value greater than all other ones of the crisp input data is at least three times larger than another one of the crisp input data having a value less than all other ones of the crisp input data.

7.   (Original) The method of claim 5, further comprising:

accepting only ones of the input data satisfying $r^2 < .0015$.

8.   (Original) The method of claim 5, wherein the obtaining of the general score comprises multiplying the distribution variance and the value of r^2.

9.   (Currently Amended) A system for managing and analyzing information obtained from ~~differential~~ expression of genetic information in biological cells, the system comprising:

a data receiver for receiving sets of expression data derived from control and treatment sets of cell-derived samples as crisp input data;

a fuzzifier for fuzzifying the crisp input data to provide fuzzified values;

a heuristic rules applier for applying a set of heuristic rules to the fuzzified values to generate a predicted value of a data point C;

a defuzzifier for defuzzifying the predicted value of C; and

a confidence level determiner for determining a confidence level of the predicted value of C.

10.   (Original) The system of claim 9, further comprising:

a filter for filtering the crisp input data to ensure the crisp data are above a predetermined noise level.

11.   (Original) The system of claim 10, wherein the heuristic rules applier uses a decision matrix.

12.   (Original) The system of claim 10, wherein the confidence level determiner comprises:

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a calculator for calculating a difference r between the defuzzified predicted value and an observed value of C; and

a squarer for squaring r to provide r^2 and for comparing r^2 to a predetermined value, a value of r^2 being smaller than the predetermined value indicating a high confidence level in the defuzzified predicted value of C.

13. (Original) The system of claim 12, wherein the confidence level determiner further comprises:

a variance determiner for determining a distribution variance of the fuzzified values; and

a scorer for obtaining a general score, for predicting credibility of decision matrix predictions, based upon the distribution variance and the value of r^2.

14. (Original) The system of claim 10, wherein the filter comprises:

an accepter for accepting the crisp input data only when one of the crisp input data having a value greater than all other ones of the crisp input data is at least three times larger than another one of the crisp input data having a value less than all other ones of the crisp input data.

15. (Original) The system of claim 13, wherein the scorer comprises a multiplier for multiplying the distribution variance and the value of r^2.

16. (Previously Presented) A machine-readable medium having recorded thereon machine-readable information, such that when the machine-readable information is read and executed by a computer, the machine-readable information causes the computer to:

receive sets of expression data derived from control and treatment sets of cell-derived samples as crisp input data, said sets of expression data representing a direction and a magnitude of regulation of each one of a higher number of different genes or proteins;

fuzzify the crisp input data to provide fuzzified values;

apply a set of heuristic rules to the fuzzified values to generate a predicted value of a data point C;

defuzzify the predicted value of C; and

determine a confidence level of the predicted value of C.

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17.   (Original) The medium of claim 16, wherein the machine-readable information further causes the computer to:

filter the crisp data to ensure the crisp data are above a predetermined noise level.

18.   (Original) The medium of claim 17, wherein the computer applies the set of heuristic rules by using a decision matrix.

19.   (Original) The medium of claim 17, wherein the machine-readable information causes the computer to determine the confidence level of the predicted value of C by:

calculating a difference r between the defuzzified predicted value and an observed value of C; and

squaring r to provide r^2 and comparing r^2 to a predetermined value, a value of r^2 being smaller than the predetermined value indicating a high confidence level in the defuzzified predicted value of C.

20.   (Original) The medium of claim 19, wherein the machine-readable information further causes the computer to determine the confidence level of the predicted value of C by:

determining a distribution variance of the fuzzified values; and

obtaining a general score, for predicting credibility of decision matrix predictions, based upon the distribution variance and the value of r^2.

21.   (Original) The medium of claim 17, wherein the machine-readable information causes the computer to filter the crisp input data by:

accepting the crisp input data only when one of the crisp input data having a value greater than all other ones of the crisp input data is at least three times larger than another one of the crisp input data having a value less than all other ones of the crisp input data.

22.   (Original) The medium of claim 20, wherein machine-readable information causes the computer to obtain the general score by multiplying the distribution variance and the value of r^2.

23.   (Previously Presented) A method of determining relationships between elements of differential gene expression data, the data being from both control sets of biological cells and

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treated sets of biological cells and reflecting a direction and magnitude of regulation of a number of different genes or proteins, comprising:

fuzzifying the differential gene expression data to produce two or more fuzzy data values;

applying a set of heuristic rules to the fuzzy data values to generate a predicted data value having a defined relationship to the two or more fuzzy data values;

defuzzifying the predicted data value to generate a crisp predicted data value; and

searching the differential gene expression data for a data value that substantially matches the crisp predicted data value.

24.   (New) A method of analysis, said method comprising:

obtaining a plurality of quantitative values based on measurements of expression level of each of a plurality of sequences of at least one of the group consisting of nucleic acids and amino acids;

based on the plurality of quantitative values, obtaining a plurality of qualitative descriptors;

based on application of a predetermined model to the plurality of qualitative descriptors, obtaining at least one predicted value, each said predicted value relating to at least one other sequence of at least one of the group consisting of nucleic acids and amino acids; and

determining a confidence level of at least one predicted value.

25.   (New) The method of analysis according to claim 24, wherein each of said plurality of quantitative values indicates a direction and a magnitude of regulation.

26.   (New) The method of analysis according to claim 24, wherein each of said plurality of quantitative values indicates a direction and a magnitude of regulation of at least one treated sample with respect to a control sample.

27.   (New) The method of analysis according to claim 24, wherein the measurements of expression level are obtained from cell-derived samples.

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28.   (New) The method of analysis according to claim 24, said method comprising determining that a predetermined relationship exists between at least one of the plurality of quantitative values and a threshold value.

29.   (New) The method of analysis according to claim 24, said method comprising determining that, among the plurality of quantitative values, a predetermined measure of variation is satisfied.

30.   (New) The method of analysis according to claim 24, wherein each of the plurality of qualitative descriptors indicates a degree of membership in at least one of a plurality of classes.

31.   (New) The method of analysis according to claim 24, wherein each of the plurality of qualitative descriptors indicates a degree of membership in each of a plurality of classes.

32.   (New) The method of analysis according to claim 24, wherein each of the plurality of qualitative descriptors indicates a distribution across a plurality of classes.

33.   (New) The method of analysis according to claim 24, wherein the predetermined model includes a set of heuristic rules.

34.   (New) The method of analysis according to claim 24, wherein the predetermined model includes a plurality of correspondences between (1) a plurality of possible relationships between at least two sets of qualitative descriptors and (2) a plurality of expected results.

35.   (New) The method of analysis according to claim 24, wherein said obtaining a predicted value includes evaluating a decision matrix.

36.   (New) The method of analysis according to claim 24, wherein said obtaining a predicted value includes inputting each of the plurality of qualitative descriptors to a corresponding dimension of a decision matrix.

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.37.   (New) The method of analysis according to claim 24, wherein said obtaining a predicted value comprises:

  based on the predetermined model, obtaining a qualitative prediction descriptor; and

  based on the qualitative prediction descriptor, obtaining the predicted value as a quantitative value.

38.   (New) The method of analysis according to claim 24, wherein the predetermined model describes a system including an activator and a repressor.

39.   (New) The method of analysis according to claim 24, wherein said determining a confidence level includes evaluating a distance between a predicted value and a corresponding observed value.

40.   (New) The method of analysis according to claim 24, wherein said confidence level is based on a measure of variance among the plurality of quantitative values.

41.   (New) The method of analysis according to claim 24, wherein said obtaining at least one predicted value comprises obtaining a plurality of predicted values,

  wherein each said predicted value corresponds to a different experimental condition, each said predicted value being based on measurements of expression level under the corresponding experimental condition.

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